MDLA_PENCA   KLQSR------DVSTSELDQFEFWVQYAAASY----------------   47

                         .**   *... ..

LIP_RHIDL   GGMTLDLPSDAPPISLSSSTNSASDGGKVVAATTAQIQEFTKYAGIAATA   150

LIP_RHIMI   YGMALNATSYPDSV------VQAMSIDGGIRAATSQEINELTYYTTLSANS   121

MDLA_PENCA   -YEADYTAQVGDKL   60

LIP_RHIDL   YCRSVVPGNKWDCVQCQKWVPDGKIITTFT-SLLSDTNGYVLRSDKQKTI   199

LIP_RHIMI   YCRTVIPGATWDCIHCDA-TEDLKIIKTWS-TLIYDTNAMVARGDSEKTI   169

MDLA_PENCA   SCSKG- - - - - - -NCPEVEA - -TGATVSYDFSDSTITDTAGYIAVDHTNSAV   102

Page 29, line 4, please rewrite the paragraph thereat as follows:

Peptide 1   **VHTGFWK (SEQ ID NO: 2)**

Peptide 2   **AWESAADELTSK (SEQ ID NO: 19)**

LIP_RHIDL   YLVFRGTNSFRSAITDIVFNFSDYKPVKGAKVHAGFLSSYEQVVNDYFPV   249

LIP_RHIMI   YIVFRGSSSIRNW IADLTFVPVSYPPVSGTKVHKGFLDSYGEVQNELVAT   219

MDLA_PENCA   VLAFRGSYSVRNWVADATFVHTNPGLCDGCLAELGFWSSWKLVRDDIIKE   152

                        . .* ***. * * . .* .*   .* . . **...   . ..

Peptide 2   IK

LIP_RHIDL   VQEQLTAHPTYKVIVTGHSLGGAQALLAGMDLYQREPRLSPKNLSIFTVG   299

LIP_RHIMI   VLDQFKQYPSYKVAVTGHSLGGATALLCALDLYQREEGLSSSNLFLYTQG   269

MDLA_PENCA   LKEVVAQNPNYELVVVGHSLGAAVATLAATDL -- RGKGYPSAKLYAYA--   198

                        . .   . * .* . * .*****.* * * . ** *.   .. . * . .

LIP_RHIDL   GPRVGNPTFAYYVESTGPFQRTVHKRDIVPHVPPQSFGFLHPGESWIK   349

LIP_RHIMI   QPRVGDPAFANYVVSTGIPYRRTVNERDIVPHLPPAAFGFLHAGEEYWIT   319

MDLA-PENCA   SPRVGNAALAKYITAQGNNF-RFTHTNDPVPKLPLLSMGYVHVSPEYWIT   247

                        * ***.... * *. .*   . * ....* **.. *   ..*.. * .* ** .

LIP_RHIDL   SGTSN – V - - - - - QICTSEIETKDCSNSIVPFTSILD – HLSYF - DINEGSC   391

LIP_RHIMI   DNSPETV - - - - - QVCTSDLETSDCSNSIVPFTSVLD – HLSYF - GINTGLC   362

MDLA_PENCA   SPNNATVSTSDIKVIDGDVSFDGNTGTGLPLLTDFEAHIWYFVQDAGKG   297

LIP_RHIDL   - - - - - - -L   392

LIP_RHIMI   - - - - - - -T   363

MDLA_PENCA   PGLPFKRV   305

Page 30, line 37, please rewrite the paragraph thereat as follows:

Degenerated primers for PCR amplification of a fragment of the lipase gene were designed based on the amino acid sequence of the isolated peptides. The following three PCR primers were synthesized:

C035: TTC CAR YTN TTY GCN CAR TGG   (SEQ ID NO: 5)

18 mer 256 mixture, based on the N-terminal sequence QLFAQW. (SEQ ID NO: 21)

C037: GCV GCH SWY TCC CAV GC   (SEQ ID NO: 6)

17 mer 216 mixture, based on internal peptide 2 sequence AWESAA (reversed). (SEQ ID NO: 22)

Page 33, line 7, please rewrite the paragraph thereat as follows:

Table 5.1. (SEQ ID NO: 13)PCR-generated putative *lipA* sequence

(The four amino acid fragments of table 5.1 are contained in SEQ ID NOS: 14-17)


```
        10         20         30         40         50         60
tacccgggntccattCAGTTGTTCGCGCAATGGTCTGCCGCAGCTTATTGCTCGAATA


              Q   L   F   A   Q   W   S   A   A   A   Y   C   S   N
        70         80         90        100        110        120


     ATATCGACTCGAAAGAVTCCAACTTGACATGCACGGCCAACGCCTGTCCATCAGTCGAGG
     N   I   D   S   K   X   S   N   L   T   C   T   A   N   A   C   P   S   V   E


        130        140        150        160        170        180
AGGCCAGTACCACGATGCTGCTGCTGGTGGAGTTCGACCTGTATGTCACTCAGATCGCAGACATAG
     E   A   S   T   T   M   L   L   E   F   D   L   Y   V   T   Q   I   A   D   I
        190        200        210        220        230        240
AGCACAGCTAATTGAACAGGACGAACGACTTTTGGAGGCACAGCCGGTTTCCTGGCCGCG
     E   H   S   -   L   N   R   T   N   D   F   W   R   H   S   R   F   P   G   R
        250        260        270        280        290        300
     G   Q   H   Q   Q   A   A   R   G   R   L   P   G   K   Q   H   D   -   E   L
```

```
            310             320             330
ATTGCTAATCYTGACTTCATCCTGGRAGATAACG
D C – X – L H P X R –  (SEQ ID NO: 13)
```

Page 37, line 10, please rewrite the paragraph thereat as follows:

The gene was sequenced using cycle sequencing and conventional sequencing technology. The complete sequence (SEQ ID NO: 18) is shown below in Table 6.1. The sequence has been determined for both strands for the complete coding region and about 100bp upstream and downstream of the coding region. The sequences downstream to the coding region have only been determined on one strand and contain a few uncertainties. In the sequence as shown below, the intron sequences are indicated as lowercase letters and the N-terminal and the two internal peptides (peptide 1 and peptide 2) are underlined:

Page 37, line 22, please rewrite the paragraph thereat as follows:

Table 6.1. (SEQ ID NO: 18) The DNA sequence for the lipA gene and flanking sequences

```
1      CCNDTTAATCCCCCACCGGGGTTCCCGCTCCCGGATGGAGATGGGGCCAAAACTGGCAAC
61     CCCCAGTTGCGCAACGGAACAACCGCCGACCCGGAACAAAGGATGCGGATGAGGAGATAC
121    GGTGCCTGATTGCATGGCTGGCTTCATCTGCTATCGTGACAGTGCTCTTTGGGTGAATAT
181    TGTTGTCTGACTTACCCCGCTTCTTGCTTTTTCCCCCCTGAGGCCCTGATGGGGAATCGC
241    GGTGGGTAATATGATATGGGTATAAAAGGGAGATCGGAGGTGCAGTTGGATTGAGGCAGT
301    GTGTGTGTGTGCATTGCAGAAGCCCGTTGGTCGCAAGGTTTTGGTCGCCTCGATTGTTTG
361    TATACCGCAAGATGTTCTCTGGACGGTTTGGAGTGCTTTTGACAGCGCTTGCTGCGCTGG
                  M   F   S   G   R   F   G   V   L   L   T   A   L   A   A   L
421    GTGCTGCCGCGCCGGCACCGCTTGCTGTGCGGAgtaggtgtgcccgatgtgagatggttg
       G   A   A   A   P   A   P   L   A   V   R
481    gatagcactgatgaagggtgaatagGTGTCTCGACTTCCACGTTGGATGAGTTGCAATTG
                              S   V   S   T   S   T   L   D   E   L   Q   L
541    TTCGCGCAATGGTCTGCCGCAGCTTATTGCTCGAATAATATCGACTCGAAAGACTCCAAC
       F   A   Q   W   S   A   A   A   Y   C   S   N   N   I   D   S   K   D   S   N
601    TTGACATGCACGGCCAACGCCTGTCCATCAGTCGAGGAGGCCAGTACCACGATGCTGCTG
       GAGTTCGACCTgtatgtcactcagatcgcagacatagagcacagctaatttgaacagGAC
       E   F   D   L
721    GAACGACTTTGGAGGCACAGCCGGTTTCCTGGCCGCGGACAACACCAACAAGCGGCTCGT
       N   D   F   G   G   T   A   G   F   L   A   A   D   N   T   N   K   R   L   V
781    GGTCGCCTTCCGGGGAAGCAGCACGATTGAGAACTGGATTGCTAATCTTGACTTCATCCT
       V   A   F   R   G   S   S   T   I   E   N   W   I   A   N   L   D   F   I   L
841    GGAAGATAACGACGACCTCTGCACCGGCTGCAAGGTCCATACTGGTTTCTGGAAGGCATG
       E   D   N   D   D   L   C   T   G   C   K   V   H   T   G   F   W   K   A   W
901    GGAGTCCGCTGCCGACGAACTGACGAGCAAGATCAAGTCTGCGATGAGCACGTATTCGGG
       E   S   A   A   D   E   L   T   S   K   I   K   S   A   M   S   T   Y   S   G
961    CTATACCCTATACTTCACCGGGCACAGTTTGGGCGGCGCATTGGCTACGCTGGGAGCGAC
       Y   T   L   Y   F   T   G   H   S   L   G   G   A   L   A   T   L   G   A   T
1021   AGTTCTGCGAAATGACGGATATAGCGTTGAGCTGGTGAGTCCTTCACAAAGGTGATGGAG
```

```
      V  L  R  N  D  G  Y  S  V  E  L
1081  CGACAATCGGGAACAGACAGTCAATAGTACACCTATGGATGTCCTCGAATCGGAAACTAT
                                    Y  T  Y  G  C  P  R  I  G  N  Y
1141  GCGCTGGCTGAGCATATCACCAGTCAGGGATCTGGGGCCAACTTCCGTGTTACACACTTG
         A  L  A  E  H  I  T  S  Q  G  S  G  A  N  F  R  V  T  H  L
1201  AACGACATCGTCCCCCGGGTGCCACCCATGGACTTTGGATTCAGTCAGCCAAGTCCGGAA
         N  D  I  V  P  R  V  P  P  M  D  F  G  F  S  Q  P  S  P  E
1261  TACTGGATCACCAGTGGCAATGGAGCCAGTGTCACGGCGTCGGATATCGAAGTCATCGAG
         Y  W  I  T  S  G  N  G  A  S  V  T  A  S  D  I  E  V  I  E
1321  GGAATCAATTCAACGGCGGGAAATGCAGGCGAAGCAACGGTGAGCGTTGTGGCTCACTTG
         G  I  N  S  T  A  G  N  A  G  E  A  T  V  S  V  V  A  H  L
1381  TGGTACTTTTTTGCGATTTCCGAGTGCCTGCTATAACTAGACCGACTGTCAGATTAGTGG
         W  Y  F  F  A  I  S  E  C  L  L  -
1441  ACGGGAGAAGTGTACATAAGTAATTAGTATATAATCAGAGCAACCCAGTGGTGGTGATGG
1501  TGGTGAAAGAAGAAACACATTGAGTTCCCATTACGKAGCAGWTAAAGCACKTKKGGAGGC
1561  GCTGGTTCCTCCACTTGGCAGTTGGCGGCCATCAATCATCTTTCCTCTCCTTACTTTCGT
1621  CCACCACAACTCCCATCCTGCCAGCTGTCGCATCCCCGGGTTGCAACAACTATCGCCTCC
1681  GGGGCCTCCGTGGTTCTCCTATATTATTCCATCCGACGGCCGACGTTTCACCCTCAACCT
1741  GCGCCGCCGCAAAATCTCCCCGAGTCGGTCAACTCCCTCGAACCGCCGCCCGCATCGACC
1801  TCACGACCCCGACCGTCTGYGATYGTCCAACCG
```

Page 39, line 1, please rewrite the table thereat as follows:

<u>Table 6.2 Alignment of the lipase 3 sequence with known fungal lipases</u>

LIPASE 3	MFSG - - - - - - - - - - RFGVLL -TALAA	-15
MDLA_PENCA	MRLS - - - - - - - - - - FETAL - SAVAS	-14
LIP_RHIDL	MVSFISISQGVSLCLLVSSMMLGSSAVPVSGKSGSSNTAVSADNAALPP	-50
LIP_RHIMI	MVLKQRANYLGFLIVFFTAFLV - - EAVPIKRQSNSTVDS- - - - - - - - - LPP	-40

LIPASE 3	L -	-16
MDLA_PENCA	L -	-15
LIP_RHIDL	LISSRCAPPSNKGSKSDLQAEPYNMQKNTEWYESHGGNLTSIGKRDDNLV	-100
LIP_RHIMI	LIPSRTSAPSSSPSTTDPEAPAM - - - - - - - - - - SRNGPLPS - - - - DVETK	-76

LIPASE 3	--------GAAAPAPLA-----------VRSVSTSTLDELQLFAQWSAAA	-47
MDLA_PENCA	--------GYALPGKLQ-------------SRDVSTSELDQFEFWVQYAAAS	-46
LIP_RHIDL	GGMTLDLPSDAPPISLSSSTNSASDGGKVVAATTAQIQEFTKYAGIAATA	-150
LIP_RHIMI	YGMALNATSYPDSV-----VQAMSIDGGIRAATSQEINELTYYTTLSANS	-121

LIPASE 3	YCSNNIDSK-DSNLTCTANACPSVEEASTTMLLEFDLTNDFGGTAGFLAA	-96
MDLA_PENCA	YYEADYTAQVGDKLSCSKGNCPEVEATGATVSYDFS-DSTITDTAGYIAV	-95
LIP_RHIDL	YCRSVVP---GNKWDCVQ—CQKWVPDGKIIT---TFTSLLSDTNGYVLR	-192
LIP_RHIMI	YCRTVIP---GATWDCIH—CDA-TEDLKIIK---TWSTLIYDTNAMVAR	-162

LIPASE 3	DNTNKRLVVAFRGSSTIENWIANLDFILEDNDDLCTGCKVHTGFWKAWES	-146
MDLA_PENCA	DHTNSAVVLAFRGSYSVRNWVADATFV-HTNPGLCDGCLAELGFWSSWKL	-144

```
LIP_RHIDL      SDKQKTIYLVFRGTNSFRSAITDIVFNFSDYKPV-KGAKVHAGFLSSYEQ      -241
LIP_RHIMI      GDSEKTIYIVFRGSSSIRNWIADLTFVPVSYPPV-SGTKVHKGFLDSYGE      -211


LIPASE 3       AADELTSKIKSAMSTYSGYTLYFTGHSLGGALATLGATVL—RNDGY-SV       -193
MDLA_PENCA     VRDDIIKELKEVVAQNPNYELVVVGHSLGAAVATLAATDL—RGKGYPSA       -192
LIP_RHIDL      VVNDYFPVVQEQLTAHPTYKVIVTGHSLGGAQALLAGMDLYQREPRLSPK      -291
LIP_RHIMI      VQNELVATVLDQFKQYPSYKVAVTGHSLGGATALLCALDLYQREEGLSSS      -261


LIPASE 3       ELYTY—GCPRIGNYALAEHITSQGSGANFRVTHLNDIVPRVPPMDFGFS       -241
MDLA_PENCA     KLYAY - - ASPRVGNAALAKYITAQGN - - NFRFTHTNDPVPKLPLLSMGYV   -238
LIP_RHIDL      NLSIFTVGGPRVGNPTFAYYVESTGIPFQ-RTVHKRDIVPHVPPQSFGFL      -340
LIP_RHIMI      NLFLYTQGQPRVGDPAFANYVVSTGIPYR-RTVNERDIVPHLPPAAFGFL      -310


LIPASE 3       QPSPEYWITSGNGASVTASDIEVIEGINSTAGNAGEATVSVV---AHLWY      -288
MDLA_PENCA     HVSPEYWITSPNNATVSTSDIKVIDGDVSFDGNTGTGLPLLTDFEAHIWY      -288
LIP_RHIDL      HPGVESWIKSGTSN-VQICTSEIE------TKDCSNSIVPETSILDHLSY      -383
LIP_RHIMI      HAGEEYWITDNSPETVQVCTSDLE------TSDCSNSIVPFTSVLDHLSY      -354


LIPASE 3       FFAISECL- - - - - - -L        -297 (SEQ ID NO: 9)
MDLA_PENCA     FVQVDAGKGPGLPFKRV         -305 (SEQ ID NO: 12)
LIP_RHIDL      F - DINEGSC- - - - - - -L      -392 (SEQ ID NO: 10)
LIP_RHIMI      F - GINTGLC- - - - - - -T      -363 (SEQ ID NO: 11)
                        *  . . .
```

Page 40, line 31, please rewrite the table thereat as follows:

Table 6.3 Alignment of coding sequence of the *lipA* gene and gene coding for mono-diacyl lipase from *Penicillium camemberti*

```
LIPASE 3       MFSGRFGVLLTALAALGAAAPAPLAVRSVSTSTLDELQLFAQWSAAAYCS      -50
               |   |  |  | | || | |   |   | ||||||         |  || |
MDLA_PENCA     MRLSFFTAL - SAVASLGYALPGKLQSRDVSTSELDQFEFWVQYAAASYYE      -49


LIPASE 3       NN I DSK – DSNLTCTANACPSVEEASTTMLLEFDLTNDFGGTAGFLAADNT    -99
                    |    |     || ||    |      |         |||    |  | |
MDLA_PENCA     ADYTAQVGDKLSCSKGNCPEVEATGATVSYDFS – DSTITDTAGY IAVDHT    -98


LIPASE 3       NKRLVVAFRGSSTIENW I ANLDFILEDNDDLCTGCKVHTGFWKAWESAAD    -149
               |   |  | |||||   || |    |      |   ||  || |||  |   |
MDLA_PENCA     NSAVVLAFRGSYSVRNWVADATFV-HTNPGLCDGCLAELGFWSSWKLVRD     -147
```

LIPASE 3	ELTSKIKSAMSTYSGYTLYFTGHSLGGALATLGATVLRNDGY-SVELYTY	-198
	| | | |||| | ||| || || || | || |	
MDLA_PENCA	DIIKELKEVVAQNPNYELVVVGHSLGAAVATLAATDLRGKGYPSAKLYAY	-197

LIPASE 3	GCPR IGNYALAEHITSQGSGANFRVTHLNDIVPRVPPMDFGFSQPSPEYW	-248
	|| || ||| || ||| || || || | | ||||| |	
MDLA_PENCA	ASPRVGNAALAKYITAQGN- - NFRFTHTNDPVPKLPLLSMGYVHVSPEYW	-245

LIPASE 3	ITSGNGASVTASDIEVIEGINSTAGNAGEATVSVV - - - AHLWYFFAISEC	-295
	||| | | | ||| || | | || | || |||	
MDLA_PENCA	ITSPNNATVSTSDIKVIDGDVSFDGNTGTGLPLLTDTFEAHIWYFVQVDAG	-295

LIPASE 3	L--------L –297 (SEQ ID NO: 9)	
MDLA_PENCA	KGPGLPFKRV –305 (SEQ ID NO: 12)	

Identity: 126 amino acids (42.42%)

Page 41, line 30, please rewrite the paragraph thereat as follows:

Table 6.4: Amino acid sequence of the precursor of lipase 3 (SEQ ID NO: 9)

```
        5        10        15        20        25        30
        |         |         |         |         |         |

  1   M F S G R F G V L L T A L A A L G A A A P A P L A V R S V S

 31   T S T L D E L Q L F A Q W S A A A Y C S N N I D S K D S N L

 61   T C T A N A C P S V E E A S T T M L L E F D L T N D F G G T

 91   A G F L A A D N T N K R L V V A F R G S S T I E N W I A N L

121   D F I L E D N D D L C T G C K V H T G F W K A W E S A A D E

151   L T S K I K S A M S T Y S G Y T L Y F T G H S L G G A L A T

181   L G A T V L R N D G Y S V E L Y T Y G C P R I G N Y A L A E

211   H I T S Q G S G A N F R V T H L N D I V P R V P P M D F G F

241   S Q P S P E Y W I T S G N G A S V T A S D I E V I E G I N S

271   T A G N A G E A T V S V V A H L W Y F F A I S E C L L
```

Number of residues: 297

Please replace the previously filed sequence listing with the enclosed papers titled -- sequence listing.--